RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _10/566, 224_

Source: _1FWP_

Date Processed by STIC: _2/3/06_

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RAW SEQUENCE LISTING   DATE: 02/03/2006
PATENT APPLICATION: US/10/566,224   TIME: 11:00:25

Input Set : **A:\PTO.TS1.txt**
Output Set: **N:\CRF4\02032006\J566224.raw**

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   3 <110> APPLICANT: FUJII, Kazutoshi
   4        IIBOSHI, Masae
   5        YANASE, Michiyo
   6        TAKATA, Hiroki
   7        TAKAHA, Takeshi
   8        KURIKI, Takashi
  10 <120> TITLE OF INVENTION: A METHOD FOR IMPROVING THE THERMOSTABILITY OF
SUCROSEPHOSPHORYLASE (SP)
  12 <130> FILE REFERENCE: EG014US
C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/566,224
C--> 15 <141> CURRENT FILING DATE: 2006-01-27
  17 <150> PRIOR APPLICATION NUMBER: JP2003-313305
  18 <151> PRIOR FILING DATE: 2003-09-04
  20 <160> NUMBER OF SEQ ID NOS: 27
  22 <170> SOFTWARE: PatentIn version 3.3
  24 <210> SEQ ID NO: 1
  25 <211> LENGTH: 1443
  26 <212> TYPE: DNA
  27 <213> ORGANISM: Streptococcus mutans
  30 <220> FEATURE:
  31 <221> NAME/KEY: CDS
  32 <222> LOCATION: (1)..(1443)
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  37 1               5                   10                  15
  39 ggt aaa aat ttg aaa gaa ttg aat gaa aat att gag aat tat ttt gga        96
  40 Gly Lys Asn Leu Lys Glu Leu Asn Glu Asn Ile Glu Asn Tyr Phe Gly
  41              20                  25                  30
  43 gat gct gtt ggc ggt gtc cat ttg ctg cca ttc ttt cct tcc aca ggt       144
  44 Asp Ala Val Gly Gly Val His Leu Leu Pro Phe Phe Pro Ser Thr Gly
  45              35                  40                  45
  47 gat cgt ggc ttt gca ccg att gat tac cat gaa gtt gac tct gct ttt       192
  48 Asp Arg Gly Phe Ala Pro Ile Asp Tyr His Glu Val Asp Ser Ala Phe
  49       50                  55                  60
  51 ggc gat tgg gat gat gtc aaa cgt ttg ggt gaa aaa tat tac ctc atg       240
  52 Gly Asp Trp Asp Asp Val Lys Arg Leu Gly Glu Lys Tyr Tyr Leu Met
  53 65                  70                  75                  80
  55 ttt gat ttc atg att aat cat att tcg cgt cag tct aaa tat tat aaa       288
  56 Phe Asp Phe Met Ile Asn His Ile Ser Arg Gln Ser Lys Tyr Tyr Lys
  57                  85                  90                  95
  59 gat tac caa gaa aag cat gaa gca agt gct tat aaa gat cta ttt tta       336
  60 Asp Tyr Gln Glu Lys His Glu Ala Ser Ala Tyr Lys Asp Leu Phe Leu
  61                 100                 105                 110
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63 aat tgg gat aaa ttt tgg cct aaa aat cgc ccg aca caa gaa gat gtg    384
64 Asn Trp Asp Lys Phe Trp Pro Lys Asn Arg Pro Thr Gln Glu Asp Val
65         115             120             125
67 gac ctg att tat aag cgt aag gat cga gca cct aag cag gaa atc caa    432
68 Asp Leu Ile Tyr Lys Arg Lys Asp Arg Ala Pro Lys Gln Glu Ile Gln
69     130             135             140
71 ttt gca gat ggc agt gtt gaa cat ctc tgg aac act ttt ggg gag gaa    480
72 Phe Ala Asp Gly Ser Val Glu His Leu Trp Asn Thr Phe Gly Glu Glu
73 145             150             155             160
75 cag att gat ctt gac gtg act aaa gaa gtg act atg gat ttt att cgc    528
76 Gln Ile Asp Leu Asp Val Thr Lys Glu Val Thr Met Asp Phe Ile Arg
77             165             170             175
79 tct acc att gaa aat tta gca gcc aac ggc tgt gat ctc att cgt ttg    576
80 Ser Thr Ile Glu Asn Leu Ala Ala Asn Gly Cys Asp Leu Ile Arg Leu
81             180             185             190
83 gat gcc ttt gct tat gct gtt aaa aag cta gat acg aat gat ttc ttt    624
84 Asp Ala Phe Ala Tyr Ala Val Lys Lys Leu Asp Thr Asn Asp Phe Phe
85         195             200             205
87 gtt gaa cct gaa atc tgg act ctg cta gat aaa gtt cgt gat ata gct    672
88 Val Glu Pro Glu Ile Trp Thr Leu Leu Asp Lys Val Arg Asp Ile Ala
89     210             215             220
91 gct gta tcg ggt gcg gaa atc ttg ccg gaa att cat gaa cac tat act    720
92 Ala Val Ser Gly Ala Glu Ile Leu Pro Glu Ile His Glu His Tyr Thr
93 225             230             235             240
95 att caa ttt aaa att gca gac cat gat tac tat gtt tat gat ttt gcc    768
96 Ile Gln Phe Lys Ile Ala Asp His Asp Tyr Tyr Val Tyr Asp Phe Ala
97             245             250             255
99 ctg cct atg gtg acg ctc tac agc cta tat tcg ggc aag gtt gac cgt    816
100 Leu Pro Met Val Thr Leu Tyr Ser Leu Tyr Ser Gly Lys Val Asp Arg
101         260             265             270
103 ctt gcc aaa tgg ctg aaa atg agt ccg atg aaa cag ttc acc acc ctt    864
104 Leu Ala Lys Trp Leu Lys Met Ser Pro Met Lys Gln Phe Thr Thr Leu
105         275             280             285
107 gat aca cat gac ggt att ggt gtg gtt gat gtt aag gat atc ctg act    912
108 Asp Thr His Asp Gly Ile Gly Val Val Asp Val Lys Asp Ile Leu Thr
109     290             295             300
111 gac gaa gaa att acc tat act tct aat gag ctt tat aag gtc ggt gcc    960
112 Asp Glu Glu Ile Thr Tyr Thr Ser Asn Glu Leu Tyr Lys Val Gly Ala
113 305             310             315             320
115 aat gtc aat cgt aag tat tca act gcc gaa tat aat aac ttg gat atc    1008
116 Asn Val Asn Arg Lys Tyr Ser Thr Ala Glu Tyr Asn Asn Leu Asp Ile
117             325             330             335
119 tat caa att aat tca act tac tat tca gca ctt ggt gat gat gat caa    1056
120 Tyr Gln Ile Asn Ser Thr Tyr Tyr Ser Ala Leu Gly Asp Asp Asp Gln
121             340             345             350
123 aaa tac ttt ttg gcc cgc ttg ata caa gct ttt gct cca ggt att cca    1104
124 Lys Tyr Phe Leu Ala Arg Leu Ile Gln Ala Phe Ala Pro Gly Ile Pro
125         355             360             365
127 cag gtt tat tac gtt ggc ttt tta gct ggc aag aat gat ctt gaa tta    1152
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128 Gln Val Tyr Tyr Val Gly Phe Leu Ala Gly Lys Asn Asp Leu Glu Leu
129     370             375             380
131 ctg gaa agc act aaa gaa ggc cgc aat atc aac cgt cat tat tat agt      1200
132 Leu Glu Ser Thr Lys Glu Gly Arg Asn Ile Asn Arg His Tyr Tyr Ser
133 385             390             395             400
135 agt gaa gaa att gct aag gaa gtg aag cgg cca gtt gtc aag gca ctt      1248
136 Ser Glu Glu Ile Ala Lys Glu Val Lys Arg Pro Val Val Lys Ala Leu
137             405             410             415
139 tta aat ctc ttt act tac cgc aat cag tca gca gct ttt gat ttg gat      1296
140 Leu Asn Leu Phe Thr Tyr Arg Asn Gln Ser Ala Ala Phe Asp Leu Asp
141             420             425             430
143 ggc cgt att gaa gtg gaa acg cca aat gaa gcg acc att gtc ata gaa      1344
144 Gly Arg Ile Glu Val Glu Thr Pro Asn Glu Ala Thr Ile Val Ile Glu
145             435             440             445
147 cgt caa aat aaa gat ggc agt cat atc gca aca gca gag att aat ctc      1392
148 Arg Gln Asn Lys Asp Gly Ser His Ile Ala Thr Ala Glu Ile Asn Leu
149     450             455             460
151 caa gat atg aca tac aga gta aca gaa aat gat caa aca ata agc ttt      1440
152 Gln Asp Met Thr Tyr Arg Val Thr Glu Asn Asp Gln Thr Ile Ser Phe
153 465             470             475             480
155 gaa                                                                  1443
156 Glu
160 <210> SEQ ID NO: 2
161 <211> LENGTH: 481
162 <212> TYPE: PRT
163 <213> ORGANISM: Streptococcus mutans
165 <400> SEQUENCE: 2
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171 Gly Lys Asn Leu Lys Glu Leu Asn Glu Asn Ile Glu Asn Tyr Phe Gly
172         20              25              30
175 Asp Ala Val Gly Gly Val His Leu Leu Pro Phe Phe Pro Ser Thr Gly
176         35              40              45
179 Asp Arg Gly Phe Ala Pro Ile Asp Tyr His Glu Val Asp Ser Ala Phe
180     50              55              60
183 Gly Asp Trp Asp Asp Val Lys Arg Leu Gly Glu Lys Tyr Tyr Leu Met
184 65              70              75              80
187 Phe Asp Phe Met Ile Asn His Ile Ser Arg Gln Ser Lys Tyr Tyr Lys
188             85              90              95
191 Asp Tyr Gln Glu Lys His Glu Ala Ser Ala Tyr Lys Asp Leu Phe Leu
192             100             105             110
195 Asn Trp Asp Lys Phe Trp Pro Lys Asn Arg Pro Thr Gln Glu Asp Val
196         115             120             125
199 Asp Leu Ile Tyr Lys Arg Lys Asp Arg Ala Pro Lys Gln Glu Ile Gln
200     130             135             140
203 Phe Ala Asp Gly Ser Val Glu His Leu Trp Asn Thr Phe Gly Glu Glu
204 145             150             155             160
207 Gln Ile Asp Leu Asp Val Thr Lys Glu Val Thr Met Asp Phe Ile Arg
208             165             170             175
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211 Ser Thr Ile Glu Asn Leu Ala Ala Asn Gly Cys Asp Leu Ile Arg Leu
212             180                 185             190
215 Asp Ala Phe Ala Tyr Ala Val Lys Lys Leu Asp Thr Asn Asp Phe Phe
216         195             200             205
219 Val Glu Pro Glu Ile Trp Thr Leu Leu Asp Lys Val Arg Asp Ile Ala
220     210             215             220
223 Ala Val Ser Gly Ala Glu Ile Leu Pro Glu Ile His Glu His Tyr Thr
224 225             230             235             240
227 Ile Gln Phe Lys Ile Ala Asp His Asp Tyr Tyr Val Tyr Asp Phe Ala
228             245             250             255
231 Leu Pro Met Val Thr Leu Tyr Ser Leu Tyr Ser Gly Lys Val Asp Arg
232         260             265             270
235 Leu Ala Lys Trp Leu Lys Met Ser Pro Met Lys Gln Phe Thr Thr Leu
236         275             280             285
239 Asp Thr His Asp Gly Ile Gly Val Val Asp Val Lys Asp Ile Leu Thr
240         290             295             300
243 Asp Glu Glu Ile Thr Tyr Thr Ser Asn Glu Leu Tyr Lys Val Gly Ala
244 305             310             315             320
247 Asn Val Asn Arg Lys Tyr Ser Thr Ala Glu Tyr Asn Asn Leu Asp Ile
248             325             330             335
251 Tyr Gln Ile Asn Ser Thr Tyr Tyr Ser Ala Leu Gly Asp Asp Asp Gln
252             340             345             350
255 Lys Tyr Phe Leu Ala Arg Leu Ile Gln Ala Phe Ala Pro Gly Ile Pro
256         355             360             365
259 Gln Val Tyr Tyr Val Gly Phe Leu Ala Gly Lys Asn Asp Leu Glu Leu
260     370             375             380
263 Leu Glu Ser Thr Lys Glu Gly Arg Asn Ile Asn Arg His Tyr Tyr Ser
264 385             390             395             400
267 Ser Glu Glu Ile Ala Lys Glu Val Lys Arg Pro Val Val Lys Ala Leu
268             405             410             415
271 Leu Asn Leu Phe Thr Tyr Arg Asn Gln Ser Ala Ala Phe Asp Leu Asp
272         420             425             430
275 Gly Arg Ile Glu Val Glu Thr Pro Asn Glu Ala Thr Ile Val Ile Glu
276     435             440             445
279 Arg Gln Asn Lys Asp Gly Ser His Ile Ala Thr Ala Glu Ile Asn Leu
280     450             455             460
283 Gln Asp Met Thr Tyr Arg Val Thr Glu Asn Asp Gln Thr Ile Ser Phe
284 465             470             475             480
287 Glu
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292 <211> LENGTH: 1434
293 <212> TYPE: DNA
294 <213> ORGANISM: Streptococcus pneumoniae
297 <220> FEATURE:
298 <221> NAME/KEY: CDS
299 <222> LOCATION: (1)..(1434)
301 <400> SEQUENCE: 3
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/566,224

DATE: 02/03/2006
TIME: 11:00:25

Input Set : A:\PTO.TS1.txt
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306  gga aat aat ctt aaa gac tta tat gat aat ttg gaa gag cat ttt gga    96
307  Gly Asn Asn Leu Lys Asp Leu Tyr Asp Asn Leu Glu Glu His Phe Gly
308                   20                  25                  30
310  gat gct att gga gga gtt cac ctt tta cca ttt ttc cca tca aca gtt    144
311  Asp Ala Ile Gly Gly Val His Leu Leu Pro Phe Phe Pro Ser Thr Val
312           35                  40                  45
314  gat cgt gga ttt gcg cca gtt gac tac gac gaa gtg gac tca gct ttt    192
315  Asp Arg Gly Phe Ala Pro Val Asp Tyr Asp Glu Val Asp Ser Ala Phe
316       50                  55                  60
318  ggt gat tgg gag gat gtg aag cgt tta ggt gag aaa tat tat ctt atg    240
319  Gly Asp Trp Glu Asp Val Lys Arg Leu Gly Glu Lys Tyr Tyr Leu Met
320  65                  70                  75                  80
322  ttt gat ttt atg att aat cat att tct cgt caa tcc aag tat tat aag    288
323  Phe Asp Phe Met Ile Asn His Ile Ser Arg Gln Ser Lys Tyr Tyr Lys
324                   85                  90                  95
326  gac tat caa gaa aaa cat gaa gcc agt gaa ttt aaa gct ctc ttt tta    336
327  Asp Tyr Gln Glu Lys His Glu Ala Ser Glu Phe Lys Ala Leu Phe Leu
328                   100                 105                 110
330  aac tgg gat aag ttt tgg cca gaa aac cgt ccg aca cag tct gat gta    384
331  Asn Trp Asp Lys Phe Trp Pro Glu Asn Arg Pro Thr Gln Ser Asp Val
332           115                 120                 125
334  gat tta att tac aag cgt aag gat cgt gca cca aag caa gag att gtg    432
335  Asp Leu Ile Tyr Lys Arg Lys Asp Arg Ala Pro Lys Gln Glu Ile Val
336       130                 135                 140
338  ttt gaa gat ggt tca gtg gaa cat ttg tgg aat acc ttt ggt gag gag    480
339  Phe Glu Asp Gly Ser Val Glu His Leu Trp Asn Thr Phe Gly Glu Glu
340  145                 150                 155                 160
342  cag att gat ctt gat gtg acc aaa gaa gta act atg gaa ttt atc cgt    528
343  Gln Ile Asp Leu Asp Val Thr Lys Glu Val Thr Met Glu Phe Ile Arg
344                   165                 170                 175
346  aag acc att cag cac ttg gca agt aat ggg tgt gat ttg att cgt cta    576
347  Lys Thr Ile Gln His Leu Ala Ser Asn Gly Cys Asp Leu Ile Arg Leu
348           180                 185                 190
350  gat gcc ttt gct tat gca gtg aag aaa ttg gat act aat gat ttc ttt    624
351  Asp Ala Phe Ala Tyr Ala Val Lys Lys Leu Asp Thr Asn Asp Phe Phe
352           195                 200                 205
354  gtg gaa cca gat att tgg gat tta ttg gac aaa gtt cga gat atc gct    672
355  Val Glu Pro Asp Ile Trp Asp Leu Leu Asp Lys Val Arg Asp Ile Ala
356       210                 215                 220
358  gct gag tat ggg aca gag ctt tta cct gag att cat gaa cac tat tcg    720
359  Ala Glu Tyr Gly Thr Glu Leu Leu Pro Glu Ile His Glu His Tyr Ser
360  225                 230                 235                 240
362  att cag ttt aaa ata gca gac cat gat tac tat gtt tat gat ttt gct    768
363  Ile Gln Phe Lys Ile Ala Asp His Asp Tyr Tyr Val Tyr Asp Phe Ala
364                   245                 250                 255
366  ctt cca atg gtg aca ctt tat act ctt tac agt tcc aga aca gag cgt    816
367  Leu Pro Met Val Thr Leu Tyr Thr Leu Tyr Ser Ser Arg Thr Glu Arg
368                   260                 265                 270
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VERIFICATION SUMMARY   DATE: 02/03/2006
PATENT APPLICATION: **US/10/566,224**   TIME: 11:00:26

Input Set : **A:\PTO.TS1.txt**
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L:14 M:270 C: Current Application Number differs, Replaced Current Application Number
L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date